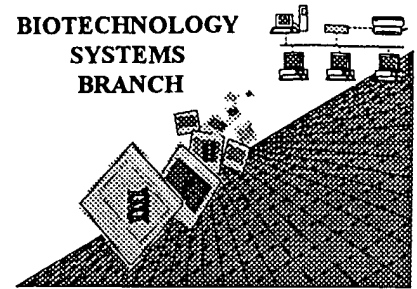


A. Gupta

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



#6

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/423,545A
Art Unit / Team No. : 1653
Date Processed by STIC: 3/29/2000

RECEIVED
APR 12 2000
TC 1600 MAIL ROOM

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/423,545A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED
APR 12 2000
TO 100 MAIL ROOM

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545ADATE: 03/29/2000
TIME: 15:44:28

Input Set: I423545A.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

1 <110> Kenji SHIBATA
2 Motoo YAMASAKI
3 Tetsuo YOSHIDA
4 Tamio MIZUKAMI
5 Akeo SHINKAI
6 Hideharu ANAZAWA
7 <120> Peptides having a cyclic structure and restoring the
8 activities of P53 protein to mutant P53 protein
9 <130> 1061
10 <140> US/09/423,545A
11 <141> 1999-11-12
12 <150> JP97/126113
13 <151> 1997-05-15
14 <160> 32

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES FOLLOW

(See item 1 on
Erra Summary Sheet)

E--> 15 <210> 8
16 <211> 32
17 <212> DNA
18 <213> Artificial Sequence
19 <220>
20 <223> Other nucleic acid Synthetic DNA
21 <400> 8
E--> 22 CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
23 32

per new sequence rules,
bases must be in

lower-case
letters

format error

→ 32

E--> 24 <210> 9
25 <211> 32
26 <212> DNA
27 <213> Artificial Sequence
28 <220>
29 <223> Other nucleic acid Synthetic DNA
30 <400> 9
E--> 31 CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
32 32

→ 32

E--> 33 <210> 10
34 <211> 26
35 <212> DNA
36 <213> Artificial Sequence
37 <220>

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545ADATE: 03/29/2000
TIME: 15:44:28

Input Set: I423545A.RAW

38 <223> Other nucleic acid Synthetic DNA
39 <400> 10
E--> 40 TCGAGAGACA TGCCTAGACA TGCCTG
41 26

42 <210> 11
E--> 43 <211> 26
44 <212> DNA
45 <213> Artificial Sequence
46 <220>
47 <223> Other nucleic acid Synthetic DNA
48 <400> 11
E--> 49 TCGACAGGCA TGTCTAGGCA TGTCTC
50 26

51 <210> 12
E--> 52 <211> 22
53 <212> DNA
54 <213> Artificial Sequence
55 <220>
56 <223> Other nucleic acid Synthetic DNA
57 <400> 12
E--> 58 TCGAGCCCGG GGGTACCGCA TG
59 22

60 <210> 13
E--> 61 <211> 14
62 <212> DNA
63 <213> Artificial Sequence
64 <220>
65 <223> Other nucleic acid Synthetic DNA
66 <400> 13
E--> 67 CGGTACCCCC GGGC
68 14

69 <210> 14
E--> 70 <211> 32
71 <212> DNA
72 <213> Artificial Sequence
73 <220>
74 <223> Other nucleic acid Synthetic DNA
75 <400> 14
E--> 76 TCGAGGGGACT TGCCTGGACT TGCCTGTCGA CG
77 32

78 <210> 15
E--> 79 <211> 32
80 <212> DNA
81 <213> Artificial Sequence
82 <220>

*same
format
env*

↓

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/423,545A

DATE: 03/29/2000

TIME: 15:44:28

Input Set: I423545A.RAW

83 <223> Other nucleic acid Synthetic DNA
84 <400> 15
E--> 85 GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
86 32

same

87 <210> 24
E--> 88 <211> 16 15 slow
89 <212> PRT
90 <213> Artificial Sequence
91 <220>
92 <221> BINDING
93 <222> (7)..(13)
94 <223> BINDING type is -CONH2-.
95 <220>
96 <221> SITE
97 <222> (15)
98 <223> Xaa represents L-Leucine amide.
99 <220>
100 <223> Synthetic peptide
101 <400> 24
W--> 102 Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser Arg His Lys Lys Xaa
103 1 5 10 15

*move amino acid nos. directly under
amino acids*

↓ FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I423545A.RAW

Line	Error/Warning	Original Text
16	E Input 32, Calc# Bases 0 differ	<211> 32
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
22	E Wrong Amino Acid Designator	CTAGACAGCC AGACTGCCTT CCGGGTCACT GC
25	E Input 32, Calc# Bases 0 differ	<211> 32
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
31	E Wrong Amino Acid Designator	CATGGCAGTG ACCCGGAAGG CAGTCTGGCT GT
34	E Input 26, Calc# Bases 0 differ	<211> 26
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
40	E Wrong Amino Acid Designator	TCGAGAGACA TGCCTAGACA TGCCTG
43	E Input 26, Calc# Bases 0 differ	<211> 26
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
49	E Wrong Amino Acid Designator	TCGACAGGCA TGTCTAGGCA TGTCTC
52	E Input 22, Calc# Bases 0 differ	<211> 22
58	E Wrong Amino Acid Designator	TCGAGCCCCG GGGTACCGCA TG
58	E Wrong Amino Acid Designator	TCGAGCCCCG GGGTACCGCA TG
58	E Wrong Amino Acid Designator	TCGAGCCCCG GGGTACCGCA TG
61	E Input 14, Calc# Bases 0 differ	<211> 14
67	E Wrong Amino Acid Designator	CGGTACCCCC GGGC
67	E Wrong Amino Acid Designator	CGGTACCCCC GGGC
70	E Input 32, Calc# Bases 0 differ	<211> 32
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
76	E Wrong Amino Acid Designator	TCGAGGGACT TGCCTGGACT TGCCTGTCGA CG
79	E Input 32, Calc# Bases 0 differ	<211> 32
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
85	E Wrong Amino Acid Designator	GTACCGTCGA CAGGCAAGTC CAGGCAAGTC CC
88	E Input 16, Calc Seq.Length 15 differ	<211> 16
102	W "N" or "Xaa" used: Feature required	Leu Lys Ser Lys Lys Gly Asp Ser Thr Ser A